EXHIBIT 14

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.
The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences",
FEMS Microbiol Lett. 174:247-250

Program [blastp]   Matrix [BLOSUM62]

Parameters used in BLASTN program only:
Reward for a match: [ ]   Penalty for a mismatch: [ ]

☐ Use Mega BLAST   Strand option [Not Applicable]

Open gap [11] and extension gap [1] penalties
gap x_dropoff [50] expect [10.0] word size [3] Filter ☑ [Align]

Sequence 1 Enter accession or GI [clone e] or download from file [ ]
or sequence in FASTA format from: [0] to: [0]

```
DYGNSPYESTDDTHADSSQPMLSISEASDMQLRSDDMDFSGDNVPHYGWQGLWSWGWAKTQ
DPEPASSATITDPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS
AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT
KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLAKLVGLYSYGDHNCHHFYTQGENLTSQGT
FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV
LVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF.
```

Sequence 2 Enter accession or GI [MOMP] or download from file [ ]
or sequence in FASTA format from: [0] to: [0]

```
cttwcaaism rmgyygarvr arviktavnk eremgealag asgnttstis
klvertnpay gkhmqdaemf tnaacmtlni wdrfdvfctl gatsgylkgn
sasfnlvglf gdgvnatkpa adsipnvqln  qsvvelytdt tawsvgara
alwecgcatl gasfqyaqsk pkieelnvlc naaeftinkp kgyvgkefpl
dltagtdaat gtkdasidyh ewqaslslsy rlnmftpyig vkwsrasfds
dtiriaqprl vtpvvdittl nptiagcgsv agantegqis dtmqivslql
nkmksrkscg iavgttivda dkyavtvetr lideraahvn aqfrf
```

[Align] [ClearInput]

Comments and suggestions to   blast-help@ncbi.nlm.nih.gov

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix [BLOSUM62] gap open: [11] gap extension: [1]

x_dropoff: [50] expect: [10.0] wordsize: [3] Filter ☑ [Align]

Sequence 1 lcl|seq_1 Length 955 *PMPE* *PTA-2462*

Sequence 2 lcl|seq_2 Length 394 *MOmP*

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment.
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Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences",
FEMS Microbiol Lett. 174:247-250

Program [blastp] [⇕]   Matrix [BLOSUM62] [⇕]

Parameters used in BLASTN program only:
Reward for a match: [_____]   **Penalty for a mismatch:** [_____]

☒ Use Mega BLAST   Strand option [Not Applicable] [⇕]

Open gap [11] and extension gap [1] penalties
gap x_dropoff [50]   expect [10.0] word size [3]   Filter ☑   [Align]

Sequence 1 Enter accession or GI [seq id 2] or download from file [_____]

or sequence in FASTA format from: [0] to: [0]

```
ALSSQPMLSISEASLNQLRSDLMDFSGLNVPHYGWQGLWIWGWARTQDPEPASSATITDPQ
KANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSAELTPSDHPFWGIT
GGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHTPSLKFSQTYTKLNERYAKNNVSSK
NYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHHFYTQGENLTSQGTFRSQTMGGAVFFDL
PMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVKGSFMNAT
QRPQAWTVELAYQPVLYRQEPGIATQLLASKGIWFGSGSPSSRHAMSYKISQQTQPLSWLT
LHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI [MOMP] or download from file [_____]

or sequence in FASTA format from: [0] to: [0]

```
cttwcaaism rmgyygarvr arviktavnk eremgealag asgnttstis
klvertnpay gkhmqdaemf tnaacmtlni wdrfdvfctl gatsgylkgn
sasfnlvglf gdgvnatkpa adsipnvqln qsvvelytdt tawsvgara
alwecgcatl gasfqyaqsk pkieelnvlc naaeftinkp kgyvgkefpl
dltagtdaat gtkdasidyh ewqaslslsy rlnmftpyig vkwsrasfds
dtiriaqprl vtpvvdittl nptiagcgsv agantegqis dtmqivslql
nkmksrkscg iavgttivda dkyavtvetr lideraahvn aqfrf
```

[Align]   [Clear Input]

Comments and suggestions to   blast-help@ncbi.nlm.nih.gov

NCBI
Blast 2 Sequ nces results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix `BLOSUM62` gap open: `11` gap extension: `1`
x_dropoff: `50` expect: `10.0` wordsize: `3` Filter ☑ `Align`

Sequence 1 lcl|seq_1   Length 965   *SEQ ID NO: 2*

Sequence 2 lcl|seq_2   Length 394   *MOMP*

No significant similarity was found